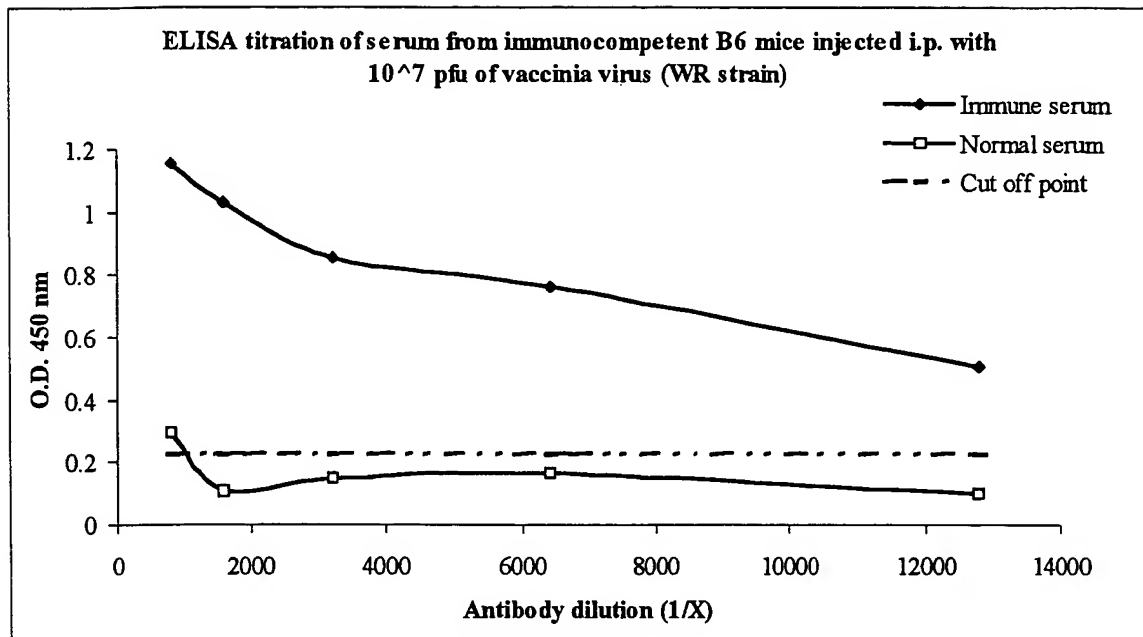
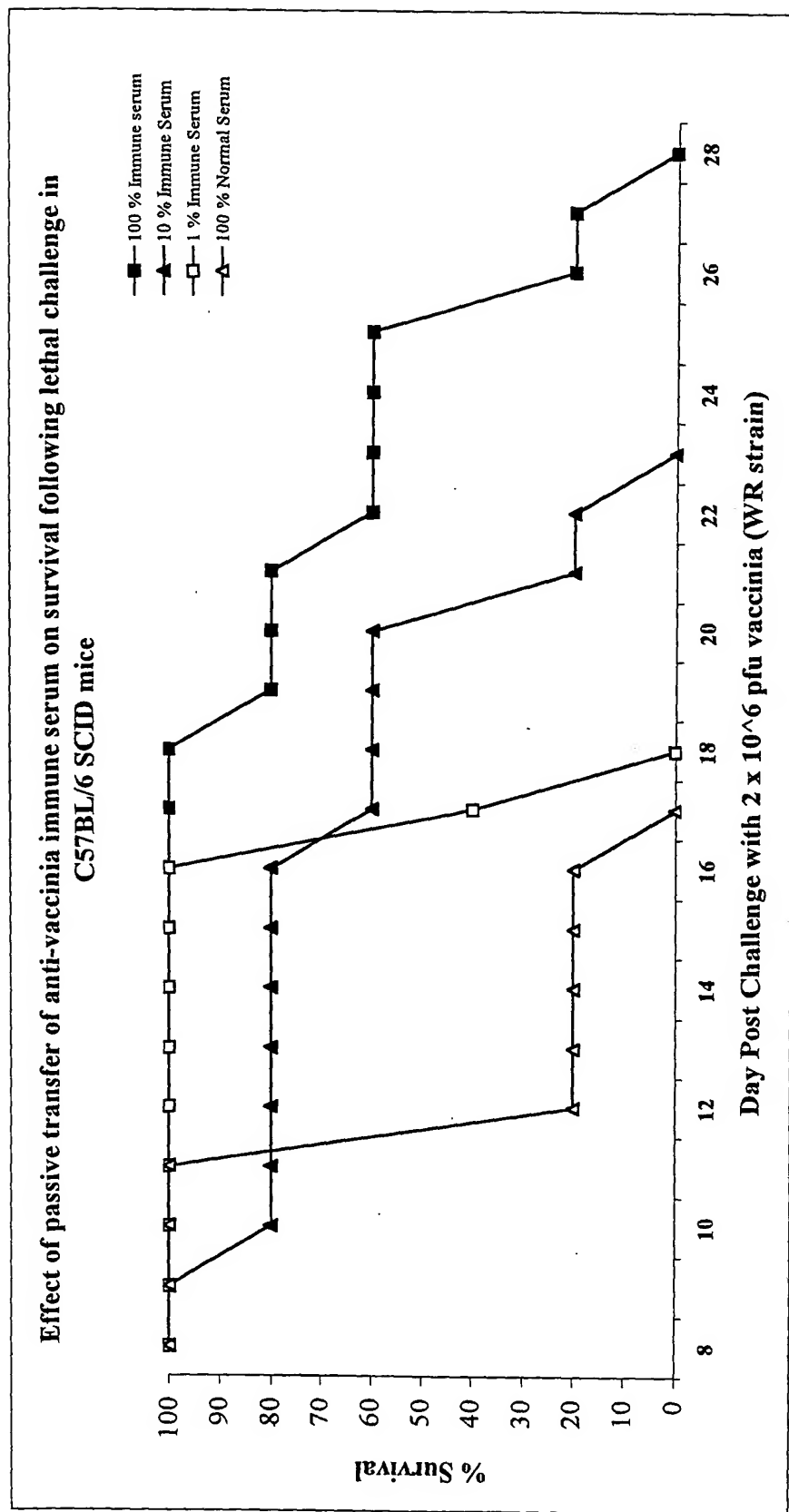


Fig 1



Wells were coated with 100 μ l of vaccinia stock (2.5×10^8 pfu per ml) diluted 1:100 in sodium bicarbonate buffer for 1 hour at 37°C. After washing three times with 0.05 % (v:v) PBS/Tween 20, the plate was blocked with 200 μ l of 10% bovine serum albumin in PBS/Tween 20 for 1 hr. The plate was again washed and 100 μ l of a two-fold dilution series of murine serum was added to triplicate wells for 1 hour at 37°C. After subsequent washing, 100 μ l of goat-anti-mouse HRP conjugated antibody diluted 1:1000 was added to each well for 1 hour at 37°C. The plate was washed again as before and 100 μ l of Sure Blue (TM) TMB peroxidase substrate (KPL, Gaithersburg, MD) was added. After allowing 5 min for color development, 100 μ l of Sure Blue (TM) stop solution was added to each well and the plate was read at 450 nm. The cut off point was defined as the mean of the data points shown for normal mouse serum + 3 standard deviations.

Fig. 2



L1R-M1Ralign

							Section 1
	(1)	1	10	20	30	40	54
L1R-P07612	(1)	MGAAASIQTTVNTLSERISSKLEQEANASAQTKCDIEIGNFYIRQNHGCNLTVK					
L1R-AAA48076	(1)	MGAAASIQTTVNTLSERISSKLEQEANASAQTKCDIEIGNFYIRQNHGCNLTVK					
M1R-AAA60821	(1)	MGAAASIQTTVNTLSERISSKLEQEANASAQTKCDIEIGNFYIRQNHGCNLTVK					
M1R-P33040	(1)	MGAAASIQTTVNTLSERISSKLEQEANASAQTKCDIEIGNFYIRQNHGCNLTVK					
Consensus	(1)	MGAAASIQTTVNTLSERISSKLEQEANASAQTKCDIEIGNFYIRQNHGCNLTVK					
							Section 2
	(55)	55	60	70	80	90	108
L1R-P07612	(55)	NMCSADADAQLDAVLSAATETYSGLTPEQKAYVPAMFTAALNIQTSVNTVVRDF					
L1R-AAA48076	(55)	NMCSADADAQLDAVLSAATETYSGLTPEQKAYVPAMFTAALNIQTSVNTVVRDF					
M1R-AAA60821	(55)	NMCSADADAQLDAVLSAATETYSGLTPEQKAYVPAMFTAALNIQTSVNTVVRDF					
M1R-P33040	(55)	NMCSADADAQLDAVLSAATETYSGLTPEQKAYVPAMFTAALNIQTSVNTVVRDF					
Consensus	(55)	NMCSADADAQLDAVLSAATETYSGLTPEQKAYVPAMFTAALNIQTSVNTVVRDF					
							Section 3
	(109)	109	120	130	140	150	162
L1R-P07612	(109)	ENYVKQTCNSSAVVDNKLKIQNVIIIDECYGAPGSPTNLEFINTGSSKGNCAIKA					
L1R-AAA48076	(109)	ENYVKQTCNSSAVVDNKLKIQNVIIIDECYGAPGSPTNLEFINTGSSKGNCAIKA					
M1R-AAA60821	(109)	ENYVKQTCNSSAVVDNKLKIQNVIIIDECYGAPGSPTNLEFINTGSSKGNCAIKA					
M1R-P33040	(109)	ENYVKQTCNSSAVVDNKLKIQNVIIIDECYGAPGSPTNLEFINTGSSKGNCAIKA					
Consensus	(109)	ENYVKQTCNSSAVVDNKLKIQNVIIIDECYGAPGSPTNLEFINTGSSKGNCAIKA					
							Section 4
	(163)	163	170	180	190	200	216
L1R-P07612	(163)	LMQLTTKATTQIAPRQVAGTGVQFYMIVIGVIIAALFMYYAKRMLFTSTNDKI					
L1R-AAA48076	(163)	LMQLTTKATTQIAPRQVAGTGVQFYMIVIGVIIAALFMYYAKRMLFTSTNDKI					
M1R-AAA60821	(163)	LMQLTTKATTQIAPRQVAGTGVQFYMIVIGVIIAALFMYYAKRMLFTSTNDKI					
M1R-P33040	(163)	LMQLTTKATTQIAPRQVAGTGVQFYMIVIGVIIAALFMYYAKRMLFTSTNDKI					
Consensus	(163)	LMQLTTKATTQIAPRQVAGTGVQFYMIVIGVIIAALFMYYAKRMLFTSTNDKI					
							Section 5
	(217)	217	230	240	250		
L1R-P07612	(217)	KLILANKENVHWTTYMDTFFRTSPMVIATTD MQN					
L1R-AAA48076	(217)	KLILANKENVHWTTYMDTFFRTSPMVIATTD MQN					
M1R-AAA60821	(217)	KLILANKENVHWTTYMDTFFRTSPMVIATTD IQN					
M1R-P33040	(217)	KLILANKENVHWTTYMDTFFRTSPMVIATTD IQN					
Consensus	(217)	KLILANKENVHWTTYMDTFFRTSPMVIATTD MQN					

FIGURE 3.

Section 1									
	(1)	1	10	20	30	40	54		
A27L-P11258	(1)	MDGTLFPGDDDLAIPATEFFSTKAAKKPDRKREQIVKADEDDNEETLKQRLTNL							
A27L-P20535	(1)	MDGTLFPGDDDLAIPATEFFSTKADKKPEAKREAIVKADEDDNEETLKQRLTNL							
A30L-P33816	(1)	MDGTLFPGDDDLAIPATEFFSTKAAKKPEAKREAIVKADGDDNEETLKQRLTNL							
A30L-AAA60882	(1)	MDGTLFPGDDDLAIPATEFFSTKAAKKPEAKREAIVKADGDDNEETLKQRLTNL							
Consensus	(1)	MDGTLFPGDDDLAIPATEFFSTKAAKKPEAKREAIVKADGDDNEETLKQRLTNL							
Section 2									
	(55)	55	60	70	80	90	108		
A27L-P11258	(55)	EKKITNVTTKFEQIEKCCCKRNDEVLFRLNHAETLRAAMISLAKKIDVQTGRRP							
A27L-P20535	(55)	EKKITNVTTKFEQIEKCCCKRNDEVLFRLNHAETLRAAMISLAKKIDVQTGRRP							
A30L-P33816	(55)	EKKITNVTTKFEQIEKCCCKRNDDVLFRLNHAETLRAAMISLAKKIDVQTGRRP							
A30L-AAA60882	(55)	EKKITNVTTKFEQIEKCCCKRNDDVLFRLNHAETLRAAMISLAKKIDVQTGRRP							
Consensus	(55)	EKKITNVTTKFEQIEKCCCKRNDDVLFRLNHAETLRAAMISLAKKIDVQTGRRP							
Section 3									
	(109)	109							
A27L-P11258	(109)	YE							
A27L-P20535	(109)	YE							
A30L-P33816	(109)	YE							
A30L-AAA60882	(109)	YE							
Consensus	(109)	YE							

FIGURE 4

Section 1							
	(1)	10	20	30	40	54	
A33R-H42520	(1)	MMTPENDEEQTSVFSATVYGDKIQQGNKRKRKRVIGLCIRISMVISLLSMITMSAF					
A33R-AAA48160	(1)	MMTPENDEEQTSVFSATVYGDKIQQGNKRKRKRVIGLCIRISMVISLLSMITMSAF					
A36R-P33850	(1)	MMTPENDEEQTSVFSATVYGDKIQQGNKRKRKRVIGICIRISMVISLLSMITMSAF					
A36R-AAA60888	(1)	MMTPENDEEQTSVFSATVYGDKIQQGNKRKRKRVIGICIRISMVISLLSMITMSAF					
Consensus	(1)	MMTPENDEEQTSVFSATVYGDKIQQGNKRKRKRVIGICIRISMVISLLSMITMSAF					
Section 2							
	(55)	55	60	70	80	90	108
A33R-H42520	(55)	LIVRLNQCMSANEAAITDAAVAVAAASSTHRKVASSTTQYDHKESCNGLYYQGS					
A33R-AAA48160	(55)	LIVRLNQCMSANEAAITDAAVAVAAASSTHRKVASSTTQYDHKESCNGLYYQGS					
A36R-P33850	(55)	LIVRLNQCMSANEAAITD - ATAVAAALSTHRKVASSTTQYKHQESCNGLYYQGS					
A36R-AAA60888	(55)	LIVRLNQCMSANEAAITD - ATAVAAALSTHRKVASSTTQYKHQESCNGLYYQGS					
Consensus	(55)	LIVRLNQCMSANEAAITDAAVAVAAASSTHRKVASSTTQYKHQESCNGLYYQGS					
Section 3							
	(109)	109	120	130	140	150	162
A33R-H42520	(109)	CYILHSDYQLFSDAKANCTAESSTLPNKSDVLITWLIDYVEDTWGSDGNPITKT					
A33R-AAA48160	(109)	CYILHSDYQLFSDAKANCTAESSTLPNKSDVLITWLIDYVEDTWGSDGNPITKT					
A36R-P33850	(108)	CYIFHSDYQLFSDAKANCATESSTLPNKSDVLTTWLIDYVEDTWGSDGNPITKT					
A36R-AAA60888	(108)	CYIFHSDYQLFSDAKANCATESSTLPNKSDVLTTWLIDYVEDTWGSDGNPITKT					
Consensus	(109)	CYILHSDYQLFSDAKANCTTESSTLPNKSDVLTTWLIDYVEDTWGSDGNPITKT					
Section 4							
	(163)	163	170	185			
A33R-H42520	(163)	TSDYQSDSDVSQEVRYFCVKTMN					
A33R-AAA48160	(163)	TSDYQSDSDVSQEVRYFCVKTMN					
A36R-P33850	(162)	TTDYQSDSDVSQEVRYFCVKTMN					
A36R-AAA60888	(162)	TTDYQSDSDVSQEVRYFCVKTMN					
Consensus	(163)	TSDYQSDSDVSQEVRYFCVKTMN					

FIGURE 5

Section 1							
	(1)	10	20	30	40	55	
D8L-P04195	(1)	MPQQLSPINIETKKAISNARLKPLDIHYNESKPTTIQNTGKLVRLNFKGGYISGG					
D8L-AAA48107	(1)	MPQQLSPINIETKKAISNARLKPLDIHYNESKPTTIQNTGKLVRLNFKGGYISGG					
F8L-P33065	(1)	MSQQLSPINIETKKAISNARLKPLNIHYNESKPTTIQNTGKLVRLNFKGGYLSGG					
F8L-AAA60846	(1)	MSQQLSPINIETKKAISNARLKPLNIHYNESKPTTIQNTGKLVRLNFKGGYLSGG					
Consensus	(1)	MSQQLSPINIETKKAISNARLKPLNIHYNESKPTTIQNTGKLVRLNFKGGYISGG					
Section 2							
	(56)	56	70	80	90	100	110
D8L-P04195	(56)	FLPNEYVLSSLHIYWGKEDDYGSNHLIDVYKYSGEINLVHWNKKKYSSYEEAKKH					
D8L-AAA48107	(56)	FLPNEYVLSSLHIYWGKEDDYGSNHLIDVYKYSGEINLVHWNKKKYSSYEEAKKH					
F8L-P33065	(56)	FLPNEYVLSSLHIYWGKEDDYGSNHLIDVYKYSGEINLVHWNKKKYSSYEEAKKH					
F8L-AAA60846	(56)	FLPNEYVLSSLHIYWGKEDDYGSNHLIDVYKYSGEINLVHWNKKKYSSYEEAKKH					
Consensus	(56)	FLPNEYVLSSLHIYWGKEDDYGSNHLIDVYKYSGEINLVHWNKKKYSSYEEAKKH					
Section 3							
	(111)	111	120	130	140	150	165
D8L-P04195	(111)	DDGLIIISIFLQVLDHKNVYFQKIVNQLDSIRSANTSAPFDSVFYLDNLLPSKLD					
D8L-AAA48107	(111)	DDGLIIISIFLQVSDHKNVYFQKIVNQLDSIRSANTSAPFDSVFYLDNLLPSTLD					
F8L-P33065	(111)	DDGLIIISIFLQVSDHKNVYFQKIVNQLDSIRTANTSAPFDSVFYLDNLLPSKLD					
F8L-AAA60846	(111)	DDGLIIISIFLQVSDHKNVYFQKIVNQLDSIRTANTSAPFDSVFYLDNLLPSKLD					
Consensus	(111)	DDGLIIISIFLQVSDHKNVYFQKIVNQLDSIRSANTSAPFDSVFYLDNLLPSKLD					
Section 4							
	(166)	166	180	190	200	210	220
D8L-P04195	(166)	YFTYLGTTINHSADAVWIIFFTPINIHSDQLSKFRTLSSSNHDGKPHYITENYR					
D8L-AAA48107	(166)	YFTYLGTTIKHSADAVWIIFFTPINIHSDQLSKFRTLSSSNHDGKPHYITENYR					
F8L-P33065	(166)	YFKYLGTTINHSADAVWIIFFTPINIHSDQLSKFRTLSSLSNHEGKPHYITENYR					
F8L-AAA60846	(166)	YFKYLGTTINHSADAVWIIFFTPINIHSDQLSKFRTLSSLSNHEGKPHYITENYR					
Consensus	(166)	YFTYLGTTINHSADAVWIIFFTPINIHSDQLSKFRTLSSSNHDGKPHYITENYR					
Section 5							
	(221)	221	230	240	250	260	275
D8L-P04195	(221)	NPYKLNDDTQVYYSGEIIIRAATTSPARENYFMRWLSDLRETCFSYYQKYIEENKT					
D8L-AAA48107	(221)	NPYKLNDDTQVYYSGEIIIRAATTSPARENYFMRWLSDLRETCFSYYQKYIEGNKT					
F8L-P33065	(221)	NPYKLNDDTEVYYSGEIIIRAATTSPARENYFMRWLSDLRETCFSYYQKYIEGNKT					
F8L-AAA60846	(221)	NPYKLNDDTEVYYSGEIIIRAATTSPARENYFMRWLSDLRETCFSYYQKYIEGNKT					
Consensus	(221)	NPYKLNDDTQVYYSGEIIIRAATTSPARENYFMRWLSDLRETCFSYYQKYIEGNKT					
Section 6							
	(276)	276	290	304			
D8L-P04195	(276)	FAIIAIVFVFILTAILFFMSRRYSREKQN					
D8L-AAA48107	(276)	FAIIAIVFVFILTAILFLMSRRYSREKQN					
F8L-P33065	(276)	FAIIAIVFVYIILTAILFLMSRRYSREKQN					
F8L-AAA60846	(276)	FAIIAIVFVYIILTAILFLMSRRYSREKQN					
Consensus	(276)	FAIIAIVFVFILTAILFLMSRRYSREKQN					

FIGURE 6

Section 1									
	(1)	1	10	20	30	40	54		
B5R-JQ1799	(1)	MKTISVVTLLCVLP	PAVVYSTCTVPTM	NNAKLTSTETS	SFNDKQKV	TFTCDQGYHS			
B5R-D42526	(1)	MKTISVVTLLCVLP	PAVVYSTCTVPTM	NNAKLTSTETS	SFNNNQKV	TFTCDQGYHS			
B7R-NP_042219	(1)	MKTISVVTLLCVLP	PAVVYSTCTVPTM	NNAKLTSTETS	SFNDKQKV	TFTCDSGYYS			
B7R-CAA49116	(1)	MKTISVVTLLCVLP	PAVVYSTCTVPTM	NNAKLTSTETS	SFNDKQKV	TFTCDSGYYS			
B7R-G36855	(1)	MKTISVVTLLCVLP	PAVVYSTCTVPTM	NNAKLTSTETS	SFNDKQKV	TFTCDSGYYS			
B7R-2015436GX	(1)	MKTISVVTLLCVLP	PAVVYSTCTVPTM	NNAKLTSTETS	SFNDKQKV	TFTCDSGYYS			
Consensus	(1)	MKTISVVTLLCVLP	PAVVYSTCTVPTM	NNAKLTSTETS	SFNDKQKV	TFTCDSGYYS			
Section 2									
	(55)	55	60	70	80	90	108		
B5R-JQ1799	(55)	SDPNAVCETDKWKY	ENPCKKMCTVSDY	ISELYNKPLYE	VNSTMTLSC	NGETKYF			
B5R-D42526	(55)	SDPNAVCETDKWKY	ENPCKKMCTVSDY	ISELYNKPLYE	VNSTMTLSC	NGETKYF			
B7R-NP_042219	(55)	LDPNAVCETDKWKY	ENPCKKMCTVSDY	VSELYNKPLYE	NAIITLICK	DETKYF			
B7R-CAA49116	(55)	LDPNAVCETDKWKY	ENPCKKMCTVSDY	VSELYNKPLYE	NAIITLICK	DETKYF			
B7R-G36855	(55)	LDPNAVCETDKWKY	ENPCKKMCTVSDY	VSELYNKPLYE	NAIITLICK	DETKYF			
B7R-2015436GX	(55)	LDPNAVCETDKWKY	ENPCKKMCTVSDY	VSELYNKPLYE	NAIITLICK	DETKYF			
Consensus	(55)	LDPNAVCETDKWKY	ENPCKKMCTVSDY	VSELYNKPLYE	NAIITLICK	DETKYF			
Section 3									
	(109)	109	120	130	140	150	162		
B5R-JQ1799	(109)	RCEEKNGNTSWND	TVTCPNAECQPLQ	LEHGSCQPVKE	KYSFGEYMT	INCDVGYE			
B5R-D42526	(109)	RCEEKNGNTSWND	TVTCPNAECQPLQ	LEHGSCQPVKE	KYSFGEYMT	INCDVGYE			
B7R-NP_042219	(109)	RCEEKNGNTSWND	TVTCPNAECQSLQ	LDHGSCQPVKE	KYSFGEHIT	INCDVGYE			
B7R-CAA49116	(109)	RCEEKNGNTSWND	TVTCPNAECQSLQ	LDHGSCQPVKE	KYSFGEHIT	INCDVGYE			
B7R-G36855	(109)	RCEEKNGNTSWND	TVTCPNAECQSLQ	LDHGSCQPVKE	KYSFGEHIT	INCDVGYE			
B7R-2015436GX	(109)	RCEEKNGNTSWND	TVTCPNAECQSLQ	LDHGSCQPVKE	KYSFGEHIT	INCDVGYE			
Consensus	(109)	RCEEKNGNTSWND	TVTCPNAECQSLQ	LDHGSCQPVKE	KYSFGEHIT	INCDVGYE			
Section 4									
	(163)	163	170	180	190	200	216		
B5R-JQ1799	(163)	VIGASYISCTANS	WNVIPSCQQKCD	IPSLSNGLIS	GSTFSIGGVI	HLSCSGFT			
B5R-D42526	(163)	VIGASYISCTANS	WNVIPSCQQKCD	IPSLSNGLIS	GSTFSIGGVI	HLSCSGFI			
B7R-NP_042219	(163)	VIGASYITCTANS	WNVIPSCQQKCD	IPSLSNGLIS	GSTFSIGGVI	HLSCSGFI			
B7R-CAA49116	(163)	VIGASYITCTANS	WNVIPSCQQKCD	IPSLSNGLIS	GSTFSIGGVI	HLSCSGFI			
B7R-G36855	(163)	VIGASYITCTANS	WNVIPSCQQKCD	IPSLSNGLIS	GSTFSIGGVI	HLSCSGFI			
B7R-2015436GX	(163)	VIGASYITCTANS	WNVIPSCQQKCD	IPSLSNGLIS	GSTFSIGGVI	HLSCSGFI			
Consensus	(163)	VIGASYITCTANS	WNVIPSCQQKCD	IPSLSNGLIS	GSTFSIGGVI	HLSCSGFI			
Section 5									
	(217)	217	230	240	250	260	270		
B5R-JQ1799	(217)	LTGSPSSTCIDGK	WNPVLPICVRT	NEEFDPVDDG	PDDDETDL	SKLSKD	VVQYEQE		
B5R-D42526	(217)	LTGSPSSTCIDGK	WNPVLPICVRT	NEEFDPVDDG	PDDDETDL	SKLSKD	VVQYEQE		
B7R-NP_042219	(217)	LTGSPSSTCIDGK	WNPVLPICIRS	NEEFDPVEDG	PDDDETDL	SKLSKD	VVQYEQE		
B7R-CAA49116	(217)	LTGSPSSTCIDGK	WNPVLPICIRS	NEEFDPVEDG	PDDDETDL	SKLSKD	VVQYEQE		
B7R-G36855	(217)	LTGSPSSTCIDGK	WNPVLPICIRS	NEEFDPVEDG	PDDDETDL	SKLSKD	VVQYEQE		
B7R-2015436GX	(217)	LTGSPSSTCIDGK	WNPVLPICIRS	NEEFDPVEDG	PDDDETDL	SKLSKD	VVQYEQE		
Consensus	(217)	LTGSPSSTCIDGK	WNPVLPICIRS	NEEFDPVEDG	PDDDETDL	SKLSKD	VVQYEQE		

FIGURE 7

	(271)	271	280	290	300	317
B5R-JQ1799	(271)	IESLEATYHII	IIVALTIMGVIFLISVIVLVCSCDKNNDQYKFHKLLP			
B5R-D42526	(271)	IESLEATYHII	IIVALTIMGVIFLISVIVLVCSCDKNNDQYKFHKLLP			
B7R-NP_042219	(271)	IESLEATYHII	IIVALTIMGVIFLISVIVLVCSCNKNNDQYKFHKLLL			
B7R-CAA49116	(271)	IESLEATYHII	IIVALTIMGVIFLISVIVLVCSCNKNNDQYKFHKLLL			
B7R-G36855	(271)	IESLEATYHII	IIVALTIMGVIFLISVIVLVCSCNKNNDQYKFHKLLL			
B7R-2015436GX	(271)	IESLEATYHII	IIVALTIMGVIFLISVIVLVCSCNKNNDQYKFHKLLL			
Consensus	(271)	IESLEATYHII	IIVALTIMGVIFLISVIVLVCSCNKNNDQYKFHKLLL			

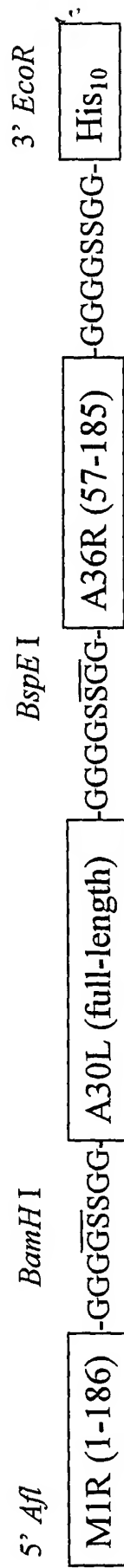
FIGURE 7 CONTINUED

H5R-I5Ralign

Section 1							
	(1)	1	10	20	30	40	55
H5R-P07242	(1)	MAWSITNKADTSSFTKMAEIRAH	LKNSAENKDKNEDI	FPEDV	IIPSTKP	PKTKRAT	
H5R-E42514	(1)	MAWSITNKADTSSFTKMAEIRAH	LKNSAENKDKNEDI	FPEDV	IIPSTKP	PKTKRAT	
I5R-P33062	(1)	MAWSITNKADTSSFTKMAEIRAH	LKNSAENKDKNDDI	FPEDV	IIPSTKP	PKTKRAT	
I5R-AAA60836	(1)	MAWSITNKADTSSFTKMAEIRAH	LKNSAENKDKNDDI	FPEDV	IIPSTKP	PKTKRAT	
Consensus	(1)	MAWSITNKADTSSFTKMAEIRAH	LKNSAENKDKNDDI	FPEDV	IIPSTKP	PKTKRAT	
Section 2							
	(56)	56	70	80	90	100	110
H5R-P07242	(56)	TPRKPAATKRSTKKEE----	VEEEV	VIEEYHQTTEKNSP----	SPGVSD	DIVESV	
H5R-E42514	(56)	TPRKPAATKRSTKKEE----	VEEEV	VIEEYHQTTEKNSP----	SPGVGD	DIVESV	
I5R-P33062	(56)	TPRKPAATKRSTKKDKKEEVEE	EEV	VIEEYHQTTEENSPPPSSSP	GVGN	DIVESV	
I5R-AAA60836	(56)	TPRKPAATKRSTKKDKKEEV-	EEV	VIEEYHQTTEENSPPPSSSP	GVGD	DIVESV	
Consensus	(56)	TPRKPAATKRSTKKDKKEEV	VEE	VIEEYHQTTEKNSPPPPSSSP	GVGD	DIVESV	
Section 3							
	(111)	111	120	130	140	150	165
H5R-P07242	(102)	AAVELDDSDGDD-----	EP	MVQVEAGKVNHSARSDLS	DLKVATDNI	VKDLK	
H5R-E42514	(102)	AAVELDDSDGDD-----	EP	MVQVEAGKVNHSARSDLS	DLKVATDNI	VKDLK	
I5R-P33062	(111)	TAVELDDSDGDDNDNDNDND	NE	PMVQVEAGKVNHSARSDLS	DLKVATDNI	VKDLK	
I5R-AAA60836	(110)	TAVELDDSDGDDNDNDNDND	NE	PMVQVEAGKVNHSARSDLS	DLKVATDNI	VKDLK	
Consensus	(111)	TAVELDDSDGDDNDNDNDND	NE	PMVQVEAGKVNHSARSDLS	DLKVATDNI	VKDLK	
Section 4							
	(166)	166	180	190	200	210	220
H5R-P07242	(148)	KIITRISAVSTVLEDVQAAGIS	RQFTSMTKAITTLSDLVTEGK	SKVVRKKVKTCK			
H5R-E42514	(148)	KIITRISAVSTVLEDVQAAGIS	RQFTSMTKAITTLSDLVTEGK	SKVVRKKVKTCK			
I5R-P33062	(166)	KIITRISAVSTVLEDVQAAGIS	RQFTSMTKSITTLSDLVTEGK	SKVVRKKVKTCK			
I5R-AAA60836	(165)	KIITRISAVSTVLEDVQAAGIS	RQFTSMTKSITTLSDLVTEGK	SKVVRKKVKTCK			
Consensus	(166)	KIITRISAVSTVLEDVQAAGIS	RQFTSMTKAITTLSDLVTEGK	SKVVRKKVKTCK			
Section 5							
	(221)	221					
H5R-P07242	(203)	K					
H5R-E42514	(203)	K					
I5R-P33062	(221)	K					
I5R-AAA60836	(220)	K					
Consensus	(221)	K					

FIGURE 8

Figure 9



Schematic representation of LAA polypeptide construct. Respective coding regions for variola virus surface proteins M1R, A30L and A36R were first amplified with PCR using vaccinia virus genome as template. PCR-based mutagenesis was carried out to convert amino acid residues to those found in variola homologs. The coding sequence for LAA was assembled by in-frame ligation of three components, M1R₁₋₁₈₆, A30L full-length and A36R₅₇₋₁₈₅, facilitated by the designed BamHI and BspEI restriction sites in the spacer-linker sequence. The 5' end of the construct has an Afl II restriction site and consensus Kozak sequence while a 10 histidine tag and EcoRI site were engineered at the 3' end of the construct.